Transcriptional Analysis of Responses of *Desulfovibrio vulgaris* to NaCl Stress Using Whole-Genome Oligonucleotide Microarrays

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The gram-negative sulfate-reducing bacterium *Desulfovibrio vulgaris* Hildenborough is fully sequenced with a genome size of 3.6 Mb and 3584 ORFs. ~~The w~~Whole-genome microarrays of *D. vulgaris* were constructed using 70-mer oligos, containing 97.1% unique probes as well as 2.9% non-specific probes that may have cross-hybridization with other ORFs. The whole genome oligonucleotide microarrays were used to explore mechanisms of *D. vulgaris* to deal with salt stress in its natural habitats.

We first examined ~~its~~ the growth of *D. vulgaris* under different concentrations of NaCl and then investigated the initial reaction to salt shock with 0.5 M NaCl. Growth of *D. vulgaris* cells was not affected significantly under 50 and 100 mM NaCl conditions. Under 250 and 500 mM NaCl conditions, they first grew slowly with about 22-hour and 42-hour lag periods, respectively, and finally they achieved 80% and 50% of the extent [not rate, I assume]of the control growth, respectively. Salt shock with 250 and 500 mM NaCl showed that *D. vulgaris* cells immediately responded to sudden increase in salinity and that their biomass decreased. *D. vulgaris* cells were not able to grow in 1000 mM NaCl medium~~a~~. There were about 370 ORFs up-regulated and around 140 ORFs down-regulated when *D. vulgaris* cells were treated with 0.5 M NaCl for 0.5 hour. For example, ORF02787, ORF02789 and ORF02792 predicted to be genes involved in glycine/betaine/L-proline transportation were up-regulated 5, 19 and 26 fold~~s~~, respectively. As expected, about 50% of those genes significantly changed ~~genes~~ were predicted to be hypothetical proteins. After a 4-hour treatment, approximately 140 ORFs were seen to be up-regulated and more than 700 ORFs, to be down-regulated. Patterns of gene expression were distinctly different among different time points.

Further study is in progress on the details of those genes significantly changed in expression ~~genes~~, ~~construction~~ on elucidation of their regulatory networks, and on the progression of ~~monitoring~~ dynamic adaptation of *D. vulgaris* cells to high salinity over time.

Question: Does “whole genome” array include the intergenic sequences? Is this array only ORFs?